

FIGURE 1

A

08/443982

CTCTAAGGTTTCGGGGTGAATCCTTGGGCCGCTGGGCAAGCGGCGAGACCTGGCCAGGGCCAGCGAGCCGAGGACAGAGGGCGCACGGAGGGCCGGG 100
CGCAGCCCCGGCGCTTGCAGACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC AGC CTG TCG AGC
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser Ser
200 Clone 15 Clone 8
AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC
Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly 412
CTA GAC CTC TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG CTC CTG CGC GAG CTG CTC
Leu Asp Leu Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg Glu Leu Leu 467
GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT 400
Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro 92
GGG GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG AAA GAT TGG AGA AGG CTG GCT CGT
Gly Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp Arg Arg Leu Ala Arg 117
CAG CTC AAA GTC TCA GAC ACC AAG ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG CGG
Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg 122
GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC
Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His Leu Val Gly Ala Leu Arg Ser 167
TGC CAG ATG AAC CTG GTG GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG AGT GGG GCC 700
Cys Gln Met Asn Leu Val Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC GAA GCG TCC TGATGGGCCGCTGCTTTGCGCTGGTGGACCACAGGC
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser *
800
ATCTACAGCCTGGACTTTGGTTCTCTCCAGGAAGGTAGCCCAGCACTGTGAAGACCCAGCAGGAAGCCAGGCTGAGTGAGCCACAGACCACCTGCTTC
900
TGAACCTAAGCTGCGTTTATTAATGCCTCTCCCGCACCAGGCCGGGCTTGGGCCCTGCACAGATATTTCCATTTCTTCTCACTATGACACTGAGCAAGA
1000
TCTTGTCTCCACTAAATGAGCTCCTGCGGGAGTAGTTGGAAGTTGGAACCGTGTCCAGCACAGAAGGAATCTGTGCAGATGAGCAGTCACACTGTTACT
1100
CCACAGCGGAGGAGACCAGCTCAGAGGCCAGGAATCGGAGCGAAGCAGAGAGGTGGAGAAGTGGGATTTGAACCCCCGCCATCCTTCACCAGAGCCCAT
1200
GCTCAACCACTGTGGCGTTCTGCTGCCCCCTGCAGTTGGCAGAAAGGATGTTTTGTCCCATTTCCTTGGAGGCCACCGGGACAGACCTGGACACTAGGGTC
1300
AGGCGGGGTGCTGTGGTGGGGAGAGGCATGGCTGGGGTGGGGTGGGGAGACCTGGTTGGCCGTGGTCCAGCTCTTGGCCCCCTGTGTGAGTTGAGTCTCC
1400
TCTCTGAGACTGCTAAGTAGGGGAGTGATGGTTGCCAGGACGAATTGAGATAATATCTGTGAGGTGCTGATGAGTGATTGACACACAGCACTCTCTAAA
1500
TCTTCCTGTGAGGATTATGGGTCTGCAATTCTACAGTTTCTTACTGTTTTGTATCAAAATCACTATCTTTCTGATAACAGAATTGCCAAGGCAGCGGG
1600
ATCTCGTATCTTTAAAAAGCAGTCTCTTATTCCTAAGGTAATCCTATTAAAA

FIGURE 2A

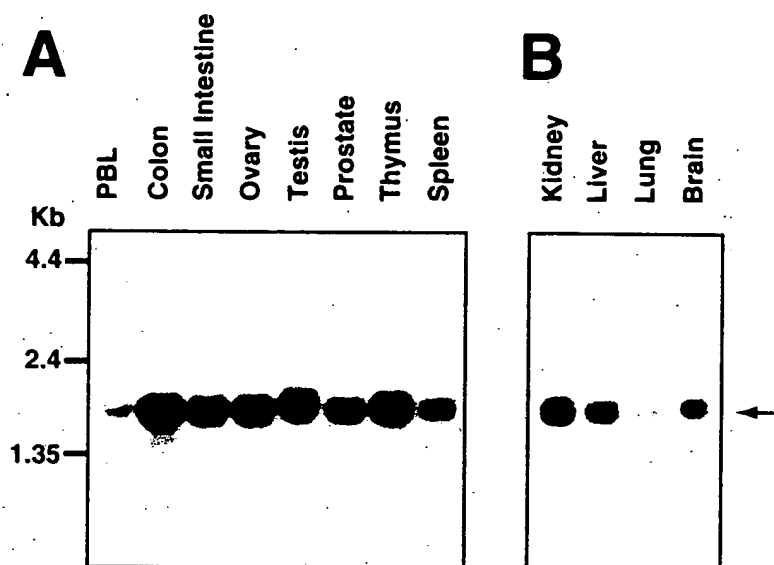
B

| | | |
|---------|-----------|---|
| hFADD | (111-145) | D E R R L A R Q L K V S D T K I D S I E D R Y P P R N L T E R V R E S L |
| rFas | (217-251) | D A K K F A P E S K I D D E I E H N S P Q D A A E Q K I Q L L L |
| hFas | (228-262) | Q V K G F V R R K N G V N E A K I D D E I K N D N V Q Q K V Q L L |
| hTNFR-1 | (341-375) | R E K E F F L S D H E I D R L E L Q N G R C L R E A Q Y S M L |



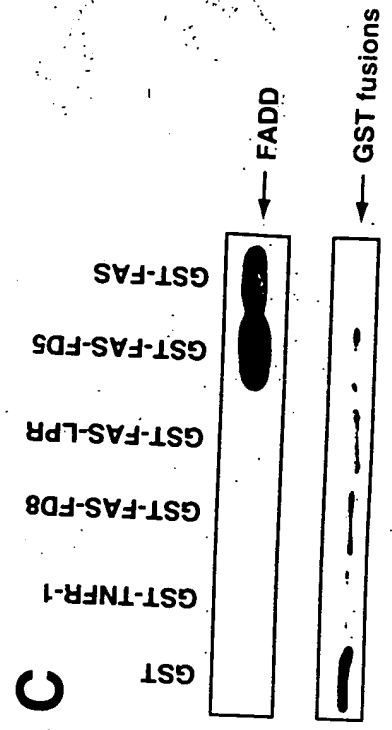
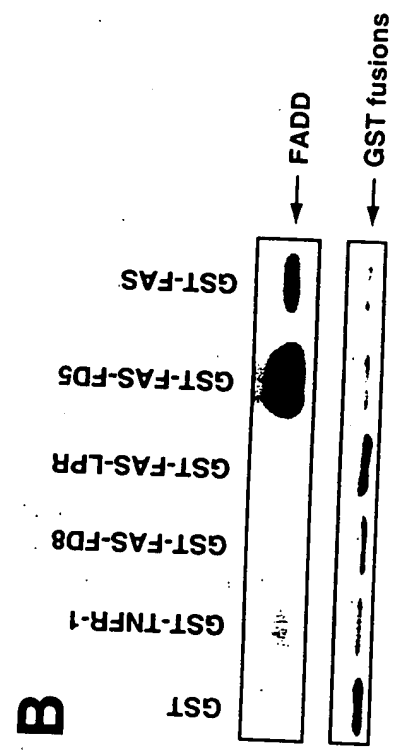
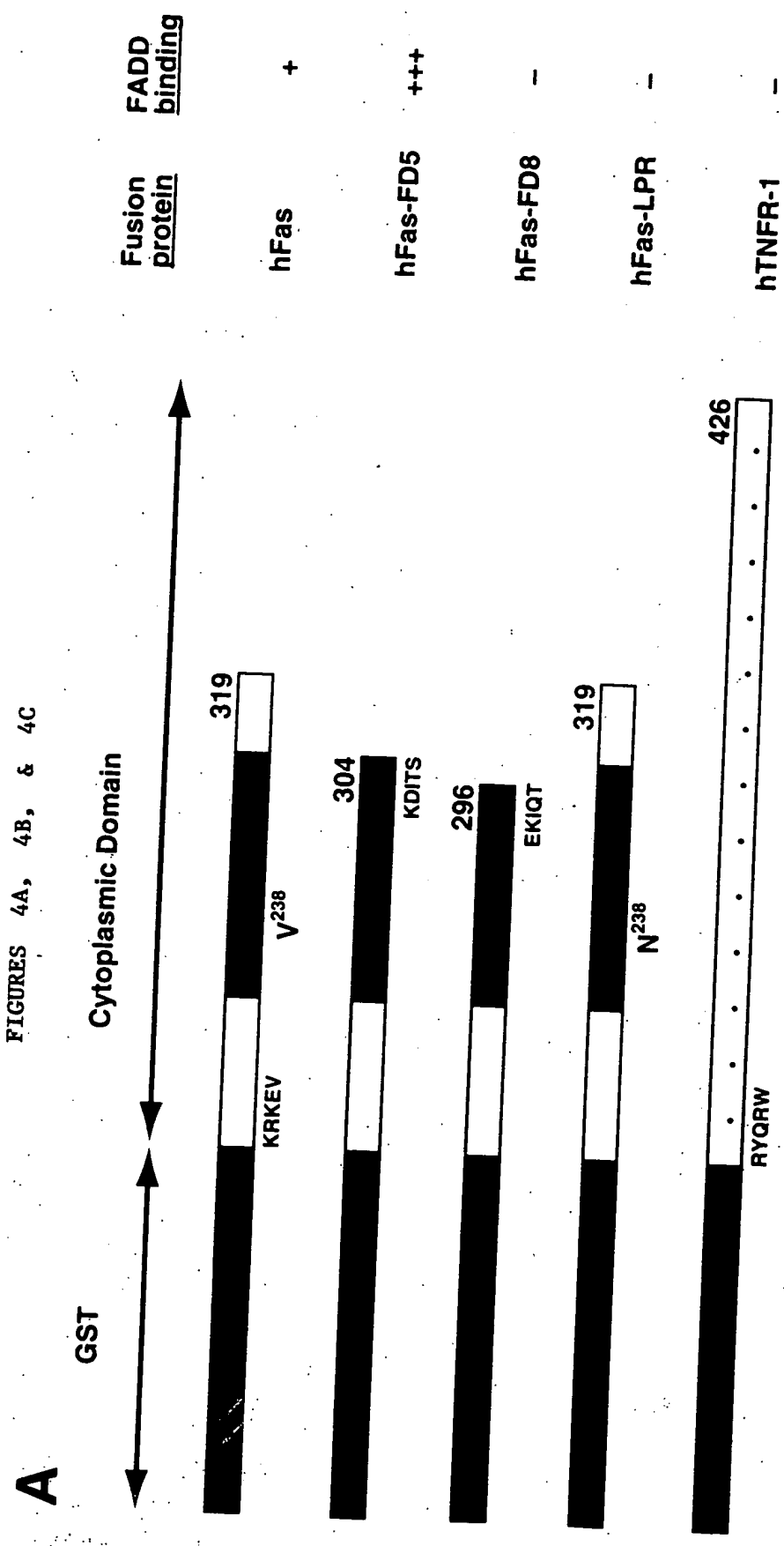
| | | |
|---------|-----------|---|
| hFADD | (146-180) | P T W F N T E K E N A T V A H L V G A L R S C Q M N L V A D L V Q E V |
| rFas | (252-286) | Q C N Y Q S H G K T G A C Q A L I Q G L R K A N R C D I A E I Q A M |
| hFas | (263-297) | P N W H Q R R T H G K K E A Y D T E L I K D L K K A N L C T L A E K I Q T I |
| hTNFR-1 | (376-410) | A T N R R R P R R R R E A T L L G R V L R R D M D L L G C L E D I E E |

FIGURE 2B



FIGURES 3A & 3B

FIGURES 4A, 4B, & 4C



A

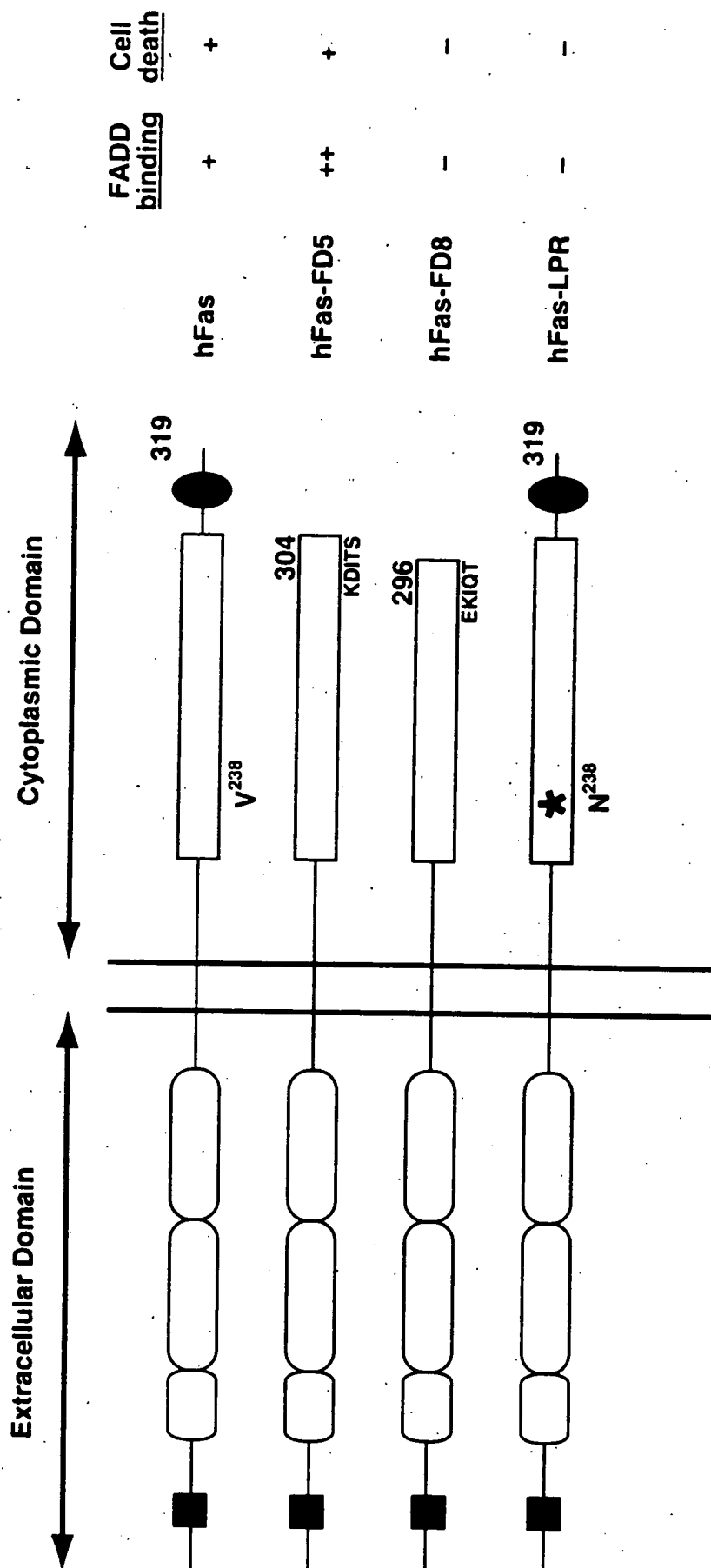
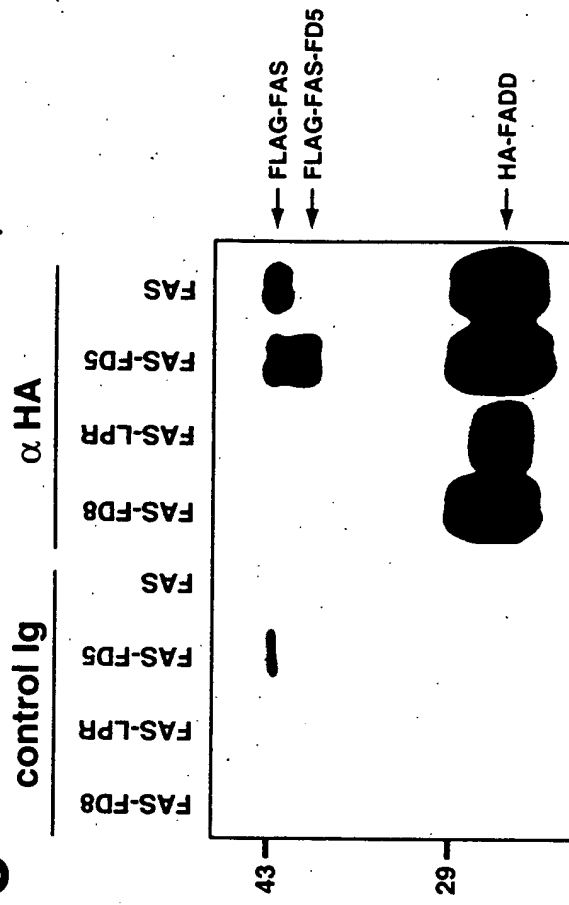
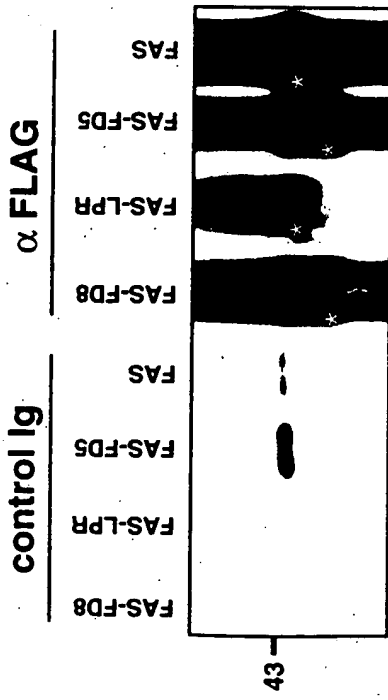


FIGURE 5A

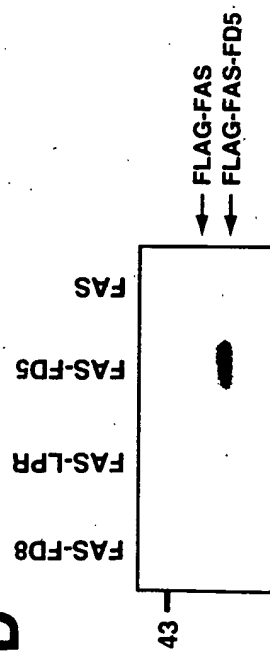
C



B



D



FIGURES 5B, 5C, & 5D

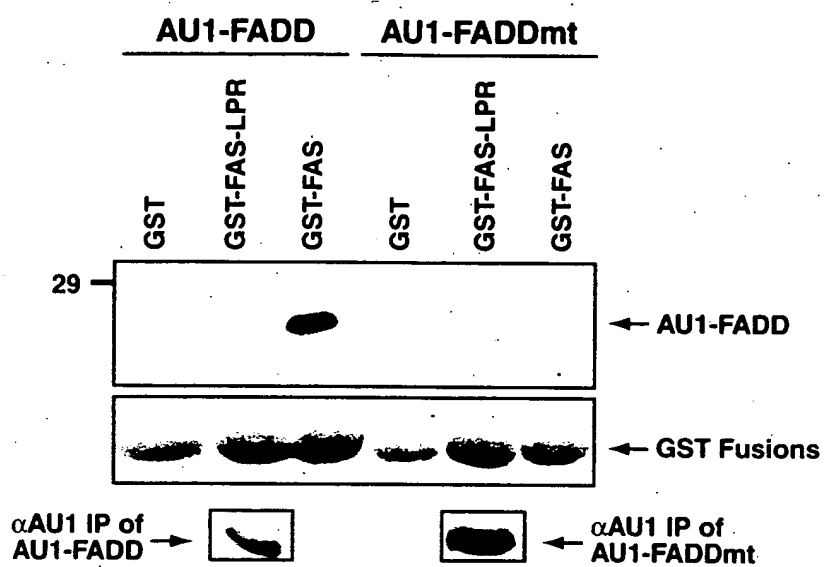
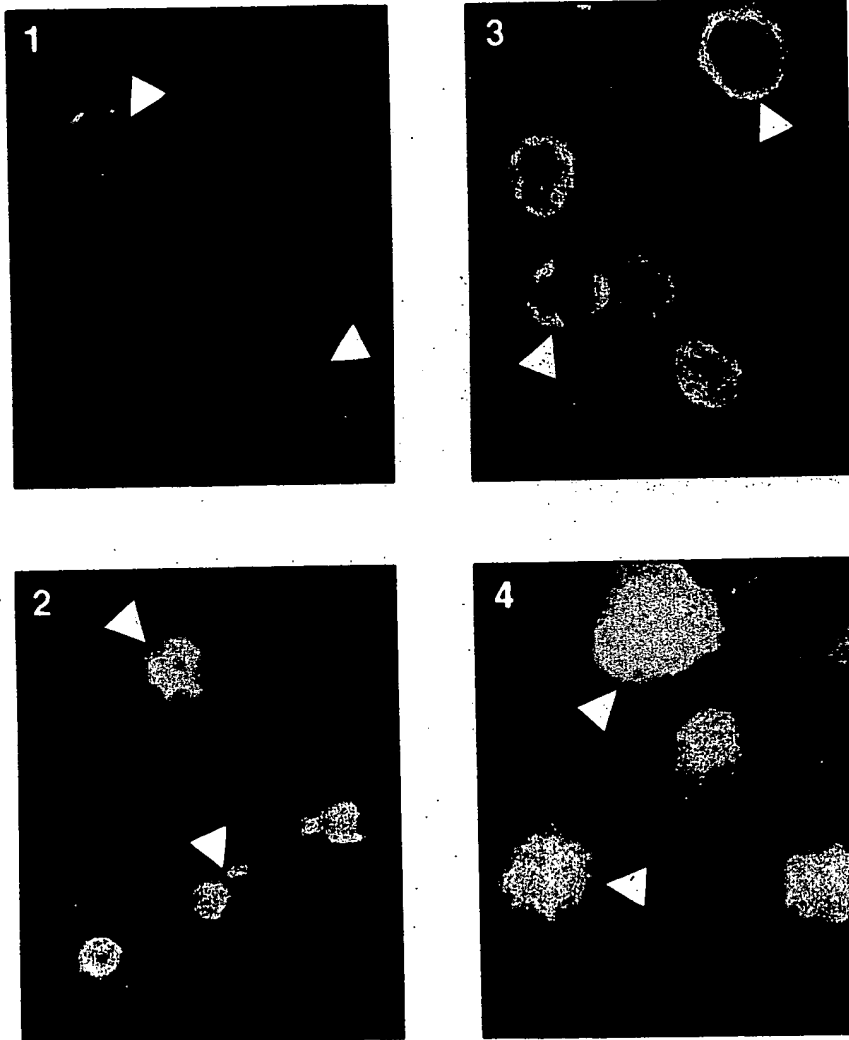


FIGURE 6

A**FIGURE 7A**

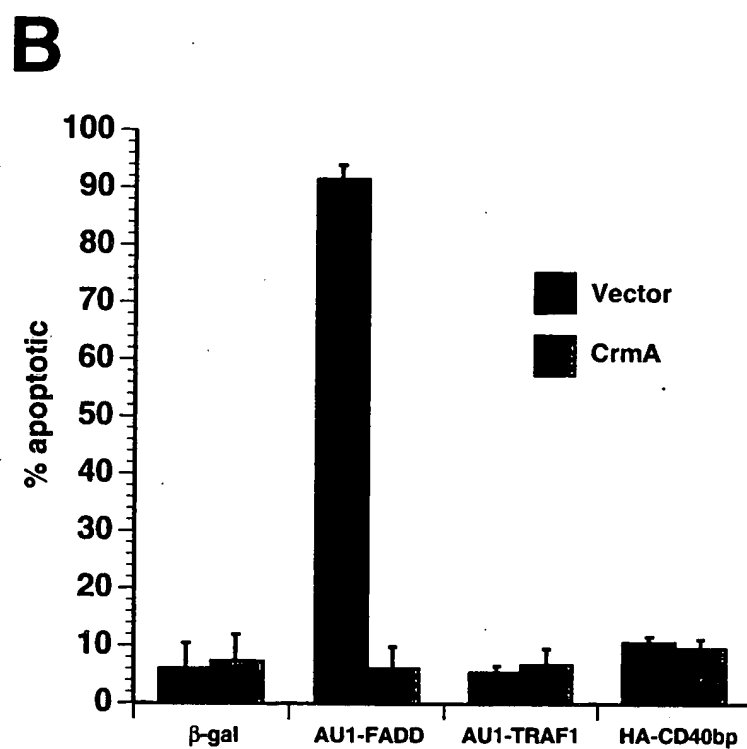


FIGURE 7B

C

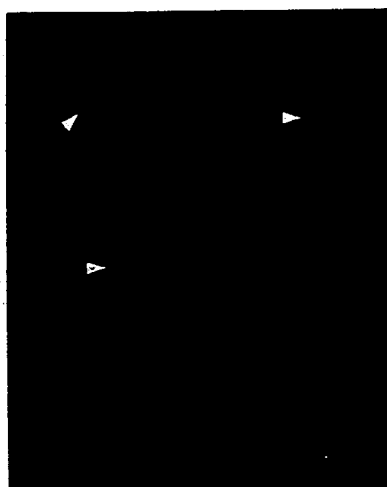


FIGURE 7C

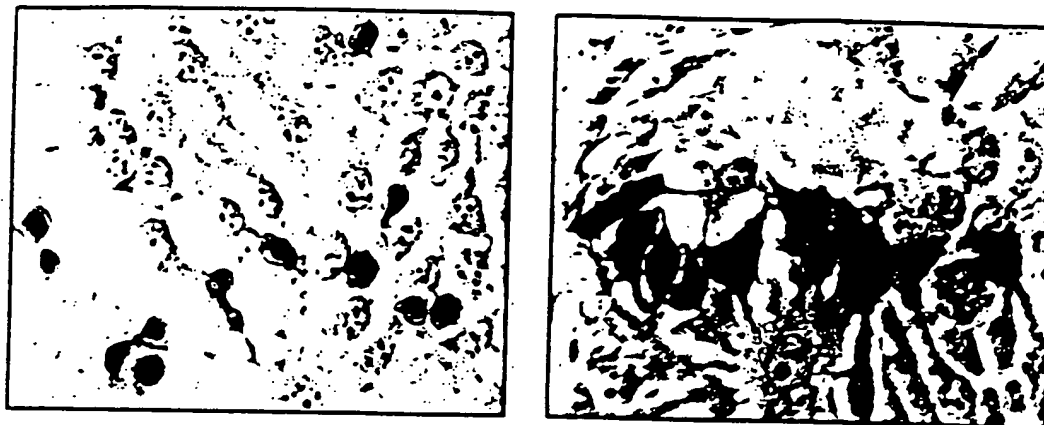
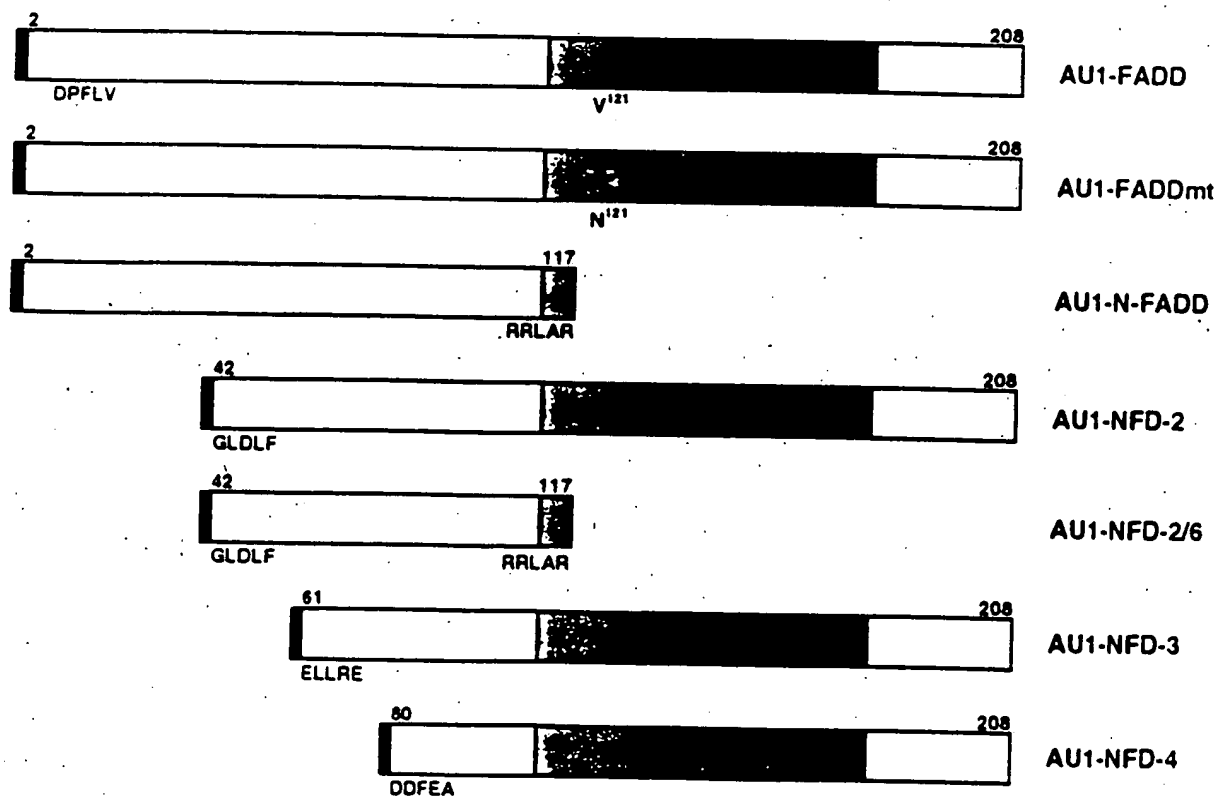
A**B****Cell
Death**

FIGURE 8A & 8B